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OM protein - protein search, using sw model

Run on: December 16, 2005, 15:16:35 ; Search time 7.58967 Seconds
(without alignments)
2484.756 Million cell updates/sec

Title: US-09-272-809-9
Perfect score: 1024
Sequence: 1 KLAVRAISRQLSPGGDIGA.....QAFGLQLMELQASLAQAEK 196
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	100.0	1112	2 S46313	phytochrome E - Ar
2	840.5	82.1	1131	2 T09701	phytochrome - Scot
3	836	81.6	1135	2 T16973	phytochrome B - cu
4	828	80.9	1132	2 T03668	phytochrome B - co
5	806	78.7	1039	2 T14802	phytochrome B - so
6	802.5	78.4	1172	1 FKMUB	phytochrome B - Ar
7	794.5	77.6	1171	2 S14085	phytochrome B - ri
8	785	76.7	1142	2 S62714	phytochrome 1b - M
9	783	76.5	1164	2 B71429	phytochrome D - Ar
10	772	75.4	1156	2 T07756	phytochrome B - so
11	765.5	74.8	1136	2 T14842	phytochrome - Norw
12	763.5	74.6	577	2 S58130	phytochrome - moss
13	763.5	74.6	1129	2 S28431	phytochrome B - po
14	747	72.9	1134	2 S31280	phytochrome - Mart
15	746	72.9	368	2 T09496	phytochrome - Doug
16	740.5	72.3	1132	2 S37206	phytochrome - moss
17	734.5	71.7	1135	2 T14803	phytochrome C - so
18	723.5	70.7	1303	1 S27396	phytochrome / prot
19	717.5	70.1	211	2 S62720	phytochrome B1 - S
20	707	69.0	210	2 S62721	phytochrome B2 - S
21	706	68.9	1111	1 FKMUC	phytochrome C - Ar
22	687	67.1	1465	2 T30891	PHY3 protein - mai
23	672	65.6	1122	1 FKMUA	phytochrome A - Ar
24	672	65.6	1122	2 D86229	phytochrome A [imp
25	671.5	65.6	1123	2 S20497	phytochrome A - po
26	669.5	65.4	1129	2 A29631	phytochrome 3 - oa
27	668.5	65.3	495	2 S00098	phytochrome 5 - oa
28	668	65.2	1129	2 S2631	phytochrome A - pa
29	666.5	65.1	1129	2 S00097	phytochrome 4 - oa

30 666 65.0 1124 1 FKPUZ phytochrome - zucc
31 665.5 65.0 1124 2 S06856 phytochrome - gard
32 665.5 65.0 1128 2 S03728 phytochrome (clone
33 662.5 64.7 1125 2 T09835 phytochrome A - po
34 660.5 64.5 1131 2 JQ0382 phytochrome A - ma
35 646 63.1 1131 2 T07137 phytochrome A - so
36 584.5 57.1 190 2 S46926 phytochrome - Mars
37 561 54.8 156 2 T14837 phytochrome 2 - No
38 548 53.5 189 2 S46927 phytochrome - Nym
39 521 50.9 197 2 S46928 phytochrome - Char
40 513 50.1 156 2 T14838 phytochrome 3 - No
41 507.5 49.6 314 2 T14865 phytochrome - Norw
42 501 48.9 156 2 T14839 phytochrome 4 - No
43 489 47.8 156 2 T14836 phytochrome - Norw
44 474 46.3 105 2 T17026 phytochrome E - ga
45 455.5 44.5 115 2 T09337 phytochrome - Doug

ALIGNMENTS

RESULT 1

S46313
Phytochrome E - Arabidopsis thaliana
N;Alternate names: protein F15J5.100
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 31-Dec-2004
C;Accession: S46313; T14813; S41912
R;Clack, T.; Mathews, S.; Sharrock, R.A.
Plant Mol. Biol. 25, 413-427, 1994
A;Title: The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the
A;Reference number: S46312; MUID:94325466; PMID:8049367
A;Accession: S46313
A;Molecule type: DNA
A;Residues: 1-1112 <CLA>
A;Cross-references: UNIPROT:P42498; UNIPARC:UPI0000131A6B; EMBL:X76610; NID:G452815; PID:
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18120
A;Accession: T14813
A;Molecule type: DNA
A;Residues: 1-1112 <BEV>
A;Cross-references: UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:F15J5.100
A;Experimental source: cultivar Columbia; BAC clone F15J5
C;Genetics:
A;Gene: PHYE; ATSP:F15J5.100
A;Map position: 4
A;Introns: 665/1; 934/2; 1032/2
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;63-569/Domain: phytochrome homology <PHYT>
F;322/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 100.0%; Score 1024; DB 2; Length 1112;
Best Local Similarity 100.0%; Pred. No. 5.5e-93;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLAVRAISRQLSPGGDIGALCTVVEDVQRLTGVDYRMVYQFHEDDHGEVVSIRSDL 60
Db 201 KLAVRAISRQLSPGGDIGALCTVVEDVQRLTGVDYRMVYQFHEDDHGEVVSIRSDL 260
Qy 61 EPYLGHLYPATDTPQAAARFLFKQNRVRMIDCNATPVKVVQSEELKPLCLVNSTLRAPH 120
Db 261 EPYLGHLYPATDTPQAAARFLFKQNRVRMIDCNATPVKVVQSEELKPLCLVNSTLRAPH 320
Qy 121 GCHTQYNNMGVSVASLALAIIVVKGKSSKLWGLVVGHCSPRYVPFPLRYACEFLMQAFG 180
Db 321 GCHTQYNNMGVSVASLALAIIVVKGKSSKLWGLVVGHCSPRYVPFPLRYACEFLMQAFG 380
Qy 181 LQLQMLQLASQLAEK 196
Db 381 LQLQMLQLASQLAEK 396

RESULT 2
T09701
phytochrome - Scotch pine
C;Species: Pinus sylvestris (Scotch pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C;Accession: T09701
R;Wiegmann-Ehrund, C.M.; Kolukisaoglu, H.U.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z16826
A;Accession: T09701
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1131 <WIE>
A;Cross-references: UNIPROT:Q41046; UNIPARC:UPI0000131A71; EMBL:X96738; NID:g1237083
A;Experimental source: isolate PSA 5.1
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;75-587/Domain: phytochrome homology <PHY>
F;332/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 82.1%; Score 840.5; DB 2; Length 1131;
Best Local Similarity 78.0%; Pred. No. 8.3e-75;
Matches 160; Conservative 15; Mismatches 21; Indels 9; Gaps 1;

QY 1 KLAVRAISRLOSLPGDGIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVSEIRSDL 60
DB 211 KLAVRAISRLOSLPGDGIGALCDTVVENVRELTYGDRVMVYKFHEDEHGEVSEIRSDL 270

QY 61 EPYLGHLHYPATDIPQARFLFKQNRVRMIDCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
DB 271 EPYLGHLHYPATDIPQARFLFKQNRVRMIDCNATPVKVIQSEELMQPLCLVGSTPSAPH 330

QY 121 GCHTOYMANNGSVASIALAIVVKGKD-----SSKLMGLVVGHHCSPPRYVFPFLRYAC 171
DB 331 GCHAOYMANNGSVASIALAIVVKGKD-----SSKLMGLVVGHHCSPPRYVFPFLRYAC 390

QY 172 CEFMQAFGLQLOMELQASOLAEK 196
DB 391 CEFMQAFGLQLOMELQASOLAEK 415

RESULT 3
T16973
phytochrome B - curled-leaved tobacco
C;Species: Nicotiana glauca (curled-leaved tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T16973
R;Hudson, M.E.; Robson, P.R.H.; Kraepiel, Y.; Caboche, M.; Smith, H.
Plant J. 12, 1091-2101, 1997
A;Title: Nicotiana glauca hlg mutants have a mutation in a PHYB-type phytochrome
A;Reference number: Z18626; MUID:98079245; PMID:9418050
A;Accession: T16973
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1135 <HUD>
A;Cross-references: UNIPROT:O24117; UNIPARC:UPI000000A9556; EMBL:Y14676; NID:g2370330; PI
A;Experimental source: cultivar PBH1d; leaf
C;Genetics:
A;Gene: PHYB
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;82-592/Domain: phytochrome homology <PHY>
F;338/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 81.6%; Score 836; DB 2; Length 1135;
Best Local Similarity 77.0%; Pred. No. 2.3e-74;
Matches 157; Conservative 18; Mismatches 21; Indels 8; Gaps 1;

QY 1 KLAVRAISRLOSLPGDGIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVSEIRSDL 60
DB 217 KLAVRAISRLOSLPGDGIGALCDTVVESVRELTYGDRVMVYKFHEDEHGEVSEIRSDL 276

QY 61 EPYLGHLHYPATDIPQARFLFKQNRVRMIDCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
DB 277 EPYLGHLHYPATDIPQARFLFKQNRVRMIDCHATPVRVVQDESLMQPLCLVGSTLRAPH 336

QY 121 GCHTOYMANNGSVASIALAIVVKGKD-----SSKLMGLVVGHHCSPPRYVFPFLRYAC 172
DB 337 GCHAOYMANNGSVASIALAIVVKGKD-----SSKLMGLVVGHHCSPPRYVFPFLRYAC 396

QY 173 EFLMQAFGLQLOMELQASOLAEK 196
DB 397 EFLMQAFGLQLOMELQASOLAEK 420

RESULT 4
T03668
phytochrome B - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T03668; T03672
R;Kern, R.; Gasch, A.; Deak, M.; Kay, S.A.; Chua, N.H.
Plant Physiol. 102, 1363-1364, 1993
A;Title: PhyB of tobacco, a new member of the photoreceptor family.
A;Reference number: Z14996; MUID:94105358; PMID:8278560
A;Accession: T03668
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1132 <KER>
A;Cross-references: UNIPROT:Z29130; UNIPARC:UPI0000131A67; EMBL:L10114; NID:g295345; PID
A;Experimental source: strain SRI; tissue-type etiolated seedling
R;Lopez-Juez, E.; Nagatani, A.; Tomizawa, K.; Deak, M.; Kern, R.; Furuya,
Plant Cell 4, 241-251, 1992
A;Title: The cucumber long hypocotyl mutant lacks a light-stable PHYB-like phytochrome.
A;Reference number: Z14997; MUID:92361250; PMID:1498594
A;Accession: T03672
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 457-506, 'S', 508-586, 'Q', 587-1132 <LOP>
A;Cross-references: UNIPARC:UPI000016DB89; EMBL:M65023; NID:g170286; PIDN:AAA34093.1; PI
C;Genetics:
A;Gene: phyb
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;80-589/Domain: phytochrome homology <PHY>
F;336/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 80.9%; Score 828; DB 2; Length 1132;
Best Local Similarity 76.5%; Pred. No. 1.4e-73;
Matches 156; Conservative 18; Mismatches 22; Indels 8; Gaps 1;

QY 1 KLAVRAISRLOSLPGDGIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVSEIRSDL 60
DB 215 KLAVRAISRLOSLPGDGIGALCDTVVESVRELTYGDRVMVYKFHEDEHGEVSEIRSDL 274

QY 61 EPYLGHLHYPATDIPQARFLFKQNRVRMIDCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
DB 275 EPYLGHLHYPATDIPQARFLFKQNRVRMIDCHATPVRVVQDESLMQPLCLVGSTLRAPH 334

QY 121 GCHTOYMANNGSVASIALAIVVKGKD-----SSKLMGLVVGHHCSPPRYVFPFLRYAC 172
DB 335 GCHAOYMANNGSVASIALAIVVKGKD-----SSKLMGLVVGHHCSPPRYVFPFLRYAC 394

QY 173 EFLMQAFGLQLOMELQASOLAEK 196
DB 395 EFLMQAFGLQLOMELQASOLAEK 418

RESULT 5
T14802
phytochrome B - sorghum (fragment)
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14802
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet,

T14842
phytochrome - Norway spruce
C/Species: Picea abies (Norway spruce)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C/Accession: T14842
R/Clapham, D.H.; Larsson, C.-T.; Qamaruddin, M.
submitted to the EMBL Data Library, June 1996
A/Description: Phytochrome from Picea abies, cDNA complete.
A/Reference number: Z18234
A/Accession: T14842
A/Status: preliminary; translated from GB/EMBL/DBEJ
A/Molecule type: mRNA
A/Residues: 1-1136 <CLA>
A/Cross-references: UNIPROT:Q40762; UNIPARC:UPI0000131A70; EMBL:U60264; NID:gl399957; PT
C/Superfamily: phytochrome, conventional type; phytochrome homology
C/Keywords: chromoprotein; photoreceptor; phytochromobilin
F:69-595/Domain: phytochrome homology <PHY>
F:336/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 74.8%; Score 765.5; DB 2; Length 1136;
Best Local Similarity 68.9%; Pred. No. 2.2e-67;
Matches 144; Conservative 23; Mismatches 29; Indels 13; Gaps 2;

Qy 1 KLAVRAISRQSLPGGDIGALCDTVVQEDVQRLTGYDRVMVYQFHEDDHGEVVSIRSDL 60
Db 215 KLAAKAIRLQALPGGDIRLLCDTVVQEVRELTGYDRVMAYRFHEDSHGEVVAEMRRPDL 274
Qy 61 EPYLGHLHPATDIPQAARFLFKQNRVMI CDCNATPVKVVQSEBELKRPCLCVNSTLRAPH 120
Db 275 EPYLGHLHPATDIPQAARFLFKQNRVMI CDCCAPPVNVIQDKRLRQPLSLCOSTLRAPH 334
Qy 121 GCHTQYMANNGSVASLALAIIV--KGKDS-----KLWGLVVGHHCSPRVYVPP 167
Db 335 GCHAQYMANNGSIASLVMSVTNENGDDSEGGGQQQPQNRRLKWLGLVVCHTSPRVYVPP 394
Qy 168 LRYACEFLMQAFLQLOQWELQLASQLAEK 196
Db 395 LRYACEFLMQVFGIQLNKEVELAAQLREK 423

RESULT 12
S58130
phytochrome - moss (Ceratodon purpureus) (fragment)
C/Species: Ceratodon purpureus
C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 31-Dec-2004
C/Accession: S58130
R/Hughes, J.; Mitmann, P.
submitted to the EMBL Data Library, July 1995
A/Description: The moss Ceratodon purpureus contains and expresses a second, conventional
A/Reference number: S58129
A/Accession: S58130
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-577 <HUG>
A/Cross-references: UNIPROT:Q39557; UNIPARC:UPI0000174E27; EMBL:X89725
C/Superfamily: phytochrome, conventional type; phytochrome homology
C/Keywords: chromoprotein; phytochromobilin
F:63-574/Domain: phytochrome homology <PHYT>
F:319/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 74.6%; Score 763.5; DB 2; Length 577;
Best Local Similarity 68.3%; Pred. No. 1.6e-67;
Matches 140; Conservative 28; Mismatches 28; Indels 9; Gaps 1;

Qy 1 KLAVRAISRQSLPGGDIGALCDTVVQEDVQRLTGYDRVMVYQFHEDDHGEVVSIRSDL 60
Db 198 KLAAKAIRLQALPGGDIRLLCDTVVQEVRELTGYDRVMAYRFHEDSHGEVVAEMRRMDL 257
Qy 61 EPYLGHLHPATDIPQAARFLFKQNRVMI CDCNATPVKVVQSEBELKRPCLCVNSTLRAPH 120
Db 258 EPYLGHLHPATDIPQAARFLFKQNRVMI ADCCASPVKLIQDDPIKQFVSLAGSTLRAPH 317
Qy 121 GCHTQYMANNGSVASLALAIIVVGKDS-----KLWGLVVGHHCSPRVYVPPFLRYA 171

